Figure S5. Distribution of acid stress genes in *ΔrfaY* over-expression library.

Distribution of acid stress response genes in the microarray result of the *ΔrfaY* over-expression library. Sorted microarray data is divided into 10 equally populated bins and number of genes belonging to "Acid Stress Response Up-regulated" category in each bin was counted and used to calculate hypergeometric *p*-value to represent the statistical significance of over-representation of those genes in that bin. The bins are pseudo-colored based on the -$\log_{10}$(*p*-value), with yellow color indicating over-representation. Generation of a similar plot has been explained in more detailed in Figure 6A.